



SEQUENCE LISTING

<110> RIEPING, MECHTHILD
BASTUCK, CHRISTINE
HERMANN, THOMAS
THIERBACH, GEORG

<120> FERMENTATIVE PROCESS FOR THE PREPARATION OF L-AMINO ACIDS
USING STRAINS OF THE FAMILY ENTEROBACTERIACEAE

<130> 21123/283665/MAS

<140> 09/963,668

<141> 2001-09-27

<150> DE 100 48 605.3

<151> 2000-09-30

<150> DE 100 55 516.0

<151> 2000-11-09

<150> DE 101 30 192.8

<151> 2001-06-22

<160> 19

<170> PatentIn Ver. 2.1

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<213> Escherichia coli

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<222> (1)..(1620)

<223> pckA

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atc agt gac gta cat gat atc gtt tac aac cca agc tac gac ctg ctg 96
Ile Ser Asp Val His Asp Ile Val Tyr Asn Pro Ser Tyr Asp Leu Leu
20 25 30

tat cag gaa gag ctc gat ccg agc ctg aca ggt tat gag cgc ggg gtg 144
Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
35 40 45

tta act aat ctg ggt gcc gtt gcc gtc gat acc ggg atc ttc acc ggt 192
Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
50 55 60

cgt tca cca aaa gat aag tat atc gtc cgt gac gat acc act cgc gat 240
Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
65 70 75 80

act ttc tgg tgg gca gac aaa ggc aaa ggt aag aac gac aac aaa cct	288
Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro	
85 90 95	
ctc tct ccg gaa acc tgg cag cat ctg aaa ggc ctg gtg acc agg cag	336
Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln	
100 105 110	
ctt tcc ggc aaa cgt ctg ttc gtt gtc gac gct ttc tgt ggt gcg aac	384
Leu Ser Gly Lys Arg Leu Phe Val Asp Ala Phe Cys Gly Ala Asn	
115 120 125	
ccg gat act cgt ctt tcc gtc cgt ttc atc acc gaa gtg gcc tgg cag	432
Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln	
130 135 140	
gcg cat ttt gtc aaa aac atg ttt att cgc ccg agc gat gaa gaa ctg	480
Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu	
145 150 155 160	
gca ggt ttc aaa cca gac ttt atc gtt atg aac ggc gcg aag tgc act	528
Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr	
165 170 175	
aac ccg cag tgg aaa gaa cag ggt ctc aac tcc gaa aac ttc gtg gcg	576
Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala	
180 185 190	
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Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly	
195 200 205	
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Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro	
210 215 220	
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ggc gat gtt gcg gtg ttc ttc ggc ctt tcc ggc acc ggt aaa acc acc	768
Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr	
245 250 255	
ctt tcc acc gac ccg aaa cgt cgc ctg att ggc gat gac gaa cac ggc	816
Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly	
260 265 270	
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Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys	
275 280 285	
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Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile	
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Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr	
325 330 335	
ccg atc tat cac atc gat aac att gtt aag ccg gtt tcc aaa gcg ggc	1056
Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly	
340 345 350	
cac gcg act aag gtt atc ttc ctg act gct gat gct ttc ggc gtg ttg	1104
His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu	
355 360 365	
ccg ccg gtt tct cgc ctg act gcc gat caa acc cag tat cac ttc ctc	1152
Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu	
370 375 380	
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Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu	
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ccg acg cca acc ttc tcc gct tgc ttc ggc gcg gca ttc ctg tcc ctg	1248
Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu	
405 410 415	
cac ccg act cag tac gca gaa gtg ctg gtg aaa cgt atg cag gcg gcg	1296
His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala	
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Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys	
435 440 445	
cgt atc tcc att aaa gat acc cgc gcc att atc gac gcc atc ctc aac	1392
Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn	
450 455 460	
ggt tcc ctg gat aat gca gaa acc ttc act ctg ccg atg ttt aac ctg	1440
Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu	
465 470 475 480	
gcg atc cca acc gaa ctg ccg ggc gta gac acg aag att ctc gat ccg	1488
Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro	
485 490 495	
cgt aac acc tac gct tct ccg gaa cag tgg cag gaa aaa gcc gaa acc	1536
Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr	
500 505 510	
ctg gcg aaa ctg ttt atc gac aac ttc gat aaa tac acc gac acc cct	1584
Leu Ala Lys Leu Phe Ile Asp Asn Phe Asp Lys Tyr Thr Asp Thr Pro	
515 520 525	

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1623

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 <211> 540
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 <213> Escherichia coli

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 35 40 45
 Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
 50 55 60
 Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
 65 70 75 80
 Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
 85 90 95
 Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
 100 105 110
 Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
 115 120 125
 Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
 130 135 140
 Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
 145 150 155 160
 Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
 165 170 175
 Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
 180 185 190
 Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
 195 200 205
 Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
 210 215 220
 Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
 225 230 235 240
 Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
 245 250 255

Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
 260 265 270
 Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
 275 280 285
 Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
 290 295 300
 Arg Arg Asp Ala Leu Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
 305 310 315 320
 Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
 325 330 335
 Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
 340 345 350
 His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
 355 360 365
 Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
 370 375 380
 Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu
 385 390 395 400
 Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
 405 410 415
 His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
 420 425 430
 Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
 435 440 445
 Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
 450 455 460
 Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu
 465 470 475 480
 Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro
 485 490 495
 Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr
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 <223> Mutagene DNA

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 <222> (1)..(35)
 <223> Technical DNA/residues of the polylinker sequence

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 <222> (36)..(522)
 <223> Part of the 5' region (pck1) of the pckA gene

<220>
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 <222> (523)..(542)
 <223> Technical DNA/residues of the polylinker sequence

<220>
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 <223> Part of the 3' region (pck2) of the pckA gene

<220>
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 <222> (1106)..(1156)
 <223> Technical DNA/residues of the polylinker sequence

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 caccaaaaga taagtatatc gtccgtgacg ataccactcg cgatactttc tgggtgggcag 180
 acaaaggcaa aggtaagaac gacaacaaac ctctctctcc ggaaacctgg cagcatctga 240
 aaggcctggg gaccaggcag ctttccggca aacgtctgtt cgttgctgac gctttctgtg 300
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 aagggttatct tccgtactgc tgatgctttc ggctgtgtgc cgccggtttc tcgcctgact 720
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 <212> DNA
 <213> Escherichia coli

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 <222> (1)..(3)
 <223> Start codon of the delta pckA allele

<220>
 <221> misc_feature
 <222> (1)..(598)
 <223> 5' region of the delta pckA allele

<220>
 <221> misc_feature
 <222> (599)..(618)
 <223> Technical DNA/residues of the polylinker sequence

<220>
 <221> misc_feature
 <222> (619)..(1291)
 <223> 3' region of the delta pckA allele

<220>
 <221> misc_feature
 <222> (1292)..(1294)
 <223> Stop codon of the delta pckA allele

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 ctgacagggtt atgagcgcgg ggtgttaact aatctgggtg ccgttgccgt cgataccggg 180
 atcttcaccg gtcgttcacc aaaagataag tatatcgctc gtgacgatac cactcgcgat 240
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 gtcgacgctt tctgtggtgc gaacccggat actcgtcttt ccgtccggtt catcaccgaa 420
 gtggcctggc aggcgcattt tgtcaaaaac atgtttatc gcccgagcga tgaagaactg 480
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 <212> DNA

<213> *Escherichia coli*

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<221> gene

<222> (376)..(714)

<223> ORF ytfP

<220>

<221> gene

<222> (461)..(727)

<223> ORF yjfa

<400> 5

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<211> 911

<212> DNA

<213> *Escherichia coli*

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<221> misc_feature

<222> (1)..(383)

<223> 5' flank of the ytfP-yjfa region

<220>

<221> misc_feature

<222> (384)..(911)

<223> 3' flank of the ytfP-yjfa region

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<221> misc_feature

<222> (376)..(378)
 <223> ATG codon of the truncated ORF ytfP

<220>
 <221> misc_feature
 <222> (388)..(390)
 <223> ATG codon of the truncated ORF yjfA

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 ccagattgtg ggtaaaatcg gcgagacgtt tggcgtaagc aatttagcgc tcgacacca 180
 gggagtaggc gactcctccc aggtagtggc cagcggctat gtattgccag gtctgcaagt 240
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 <212> DNA
 <213> Escherichia coli

<220>
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 <223> Deletion-carrying ytfP-yjfA region

<220>
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 <222> (1)..(630)
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<220>
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 <222> (631)..(1158)
 <223> 3' flank of the ytfP-yjfA region

<220>
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 <222> (376)..(378)
 <223> ATG codon of the truncated ORF ytfP

<220>
 <221> misc_feature
 <222> (635)..(637)
 <223> ATG codon of the truncated ORF yjfA

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ccagattgtg ggtaaaatcg gcgagacggt tggcgtaagc aatttagcgc tcgacaccca 180
gggagtaggc gactcctccc aggtagtggg cagcggctat gtattgccag gtctgcaagt 240
gaaatacggc gtgggtatat ttgactctat agcaacactc acgttacgtt atcgctgat 300
gcctaagcta tatctggaag ccgtgtctgg tgtagaccag gcaactggatt tgctctatca 360
gttcgagttt tagcaatgcg aatatttgtc tacggcagtt tacgccacaa acaaggcaac 420
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tacgcgcgcc agttgattca gacgcgtac tatgcatacg ccaccttcgg gtggcggtgt 660
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gcgtattacc ataaaaagat gggggaacag tgcaggtatg gtcattccca atatcgtaat 900
gaaagaactt aacttacagc cggggcagag cgtggaggcg caagtgagca acaatcaact 960
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<210> 8
<211> 20
<212> DNA
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<220>
<223> Description of the Artificial Sequence: Primer
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<210> 9
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<212> DNA
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<210> 10
<211> 22
<212> DNA
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<220>
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